STIC-Biotech/Ch mLib

61786

Fr m: STIC-ILL
Sent: Wednesday, March 06, 2002 9:19 AM
T : STIC-Biotech/ChemLib
Subject: FW: sequence search request

-----Original Message-----
From: Chernyshev, Olga
Sent: Wednesday, March 06, 2002 9:17 AM
To: STIC-ILL
Subject: sequence search request

US case 09/853,753
Please search SEQ ID NO:1 and 2.
Thank you very much!

Olga N. Chernyshev
AU1646
CM1 8D06
305-1003
mail box 10C01

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 3/7/02
Date Completed: 3/8/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 04
WWW/Internet: _____
Other (specify): _____

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 08:51:10 ; Search time 2236.97 Seconds
(without alignments)
16939.888 Million cell updates/sec

Title: US-09-853-753-1
Perfect score: 2297
Sequence: 1 ggctgagggagtggaggggg.....aaggttaaaccggtttctct 2297

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_om:*
20: em_or:*
21: em_ov:*
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23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*
28: em_un:*
29: em_vi:*
30: em_htgo_hum:*
31: em_htgo_inv:*
32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2241	97.6	2713	9	HSA278865	AJ278865 Homo sapi
3	2163	94.2	133568	9	HS169I5	Z93015 Human DNA s
4	186	8.1	1818	9	S83462	S83462 ALS=85 kda
5	183.2	8.0	37635	9	AC004152	AC004152 Homo sapi
6	173.4	7.5	2125	9	HUMIGFACID	M86826 Human IGF b
7	173.4	7.5	4574	9	AF192554	AF192554 Homo sapi
8	173.4	7.5	21419	9	HS447E6	AL031724 Human DNA
9	161.2	7.0	251997	2	AC012180	AC012180 Homo sapi
10	147.8	6.4	128318	2	AC092532	AC092532 Papio cyn
11	145.6	6.3	157419	2	AC025389	AC025389 Homo sapi
12	144.6	6.3	1907	9	AB045987	AB045987 Macaca fa
13	143	6.2	1441	9	AF283463	AF283463 Homo sapi
14	143	6.2	1782	9	BC011787	BC011787 Homo sapi
15	143	6.2	2236	6	AX047642	AX047642 Sequence
16	143	6.2	2236	6	AX055398	AX055398 Sequence
17	143	6.2	168239	9	AC007663	AC007663 Homo sapi
18	143	6.2	174840	9	AC006549	AC006549 Homo sapi
19	143	6.2	184929	9	AC058790	AC058790 Homo sapi
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21	140.2	6.1	5270	10	AF006203	AF006203 Rattus no
22	137.8	6.0	154277	2	AP003943	AP003943 Oryza sat
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24	131.2	5.7	2382	6	AX156562	AX156562 Sequence
25	131.2	5.7	2636	6	AX156560	AX156560 Sequence
26	130.4	5.7	215727	2	AC073701	AC073701 Mus muscu
27	130.2	5.7	4933	9	AB014544	AB014544 Homo sapi
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34	126	5.5	3202	10	MMU66900	U66900 Mus musculu
35	126	5.5	175759	10	AF220294	AF220294 Mus muscu
36	125.2	5.5	130730	2	AL354712	AL354712 Homo sapi
37	125.2	5.5	159802	2	AC019262	AC019262 Homo sapi
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39	124	5.4	136198	2	AP003883	AP003883 Oryza sat
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43	119.2	5.2	3573	10	RNPLGPV	Z69594 R.norvegicu
44	119	5.2	1444	9	AF371328	AF371328 Homo sapi
45	117.8	5.1	1263	6	AX149553	AX149553 Sequence

ALIGNMENTS

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LOCUS AF254868 2297 bp mRNA PRI 28-DEC-2000
DEFINITION Homo sapiens nyctalopin mRNA, complete cds.
ACCESSION AF254868
VERSION AF254868.1 GI:11993320
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2297)
AUTHORS Bech-Hansen,N.T., Naylor,M.J., Maybaum,T.A., Sparkes,R.L., Koop,B., Birch,D.G., Bergen,A.A., Prinsen,C.F., Polomeno,R.C., Gal,A., Drack,A.V., Musarella,M.A., Jacobson,S.G., Young,R.S. and Weleber,R.G.
TITLE Mutations in NYX, encoding the leucine-rich proteoglycan nyctalopin, cause X-linked complete congenital stationary night blindness
JOURNAL Nat. Genet. 26 (3), 319-323 (2000)

```
  MEDLINE   20517340
   PUBMED   11062471
REFERENCE   2  (bases 1 to 2297)
  AUTHORS   Bech-Hansen,N.T., Maybaum,T.A. and Naylor,M.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-2000) Medical Genetics, University of Calgary,
            3330 Hospital Dr. N.W., Calgary, AB T2N 4N1, Canada
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                     /db_xref="taxon:9606"
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                     LRELAAFDNLFRRVPGALRGLANLTHAHLERGRIEAVASSSLQGLRRLRSLSLQANRV
                     RAVHAGAFGDCGVLEHLLLNDNLLAELPADAFRGLRRLRTLNLGGNALDRVARAWFAD
                     LAELELLYLDRNSIAFVEEGAFQNLSGLLALHLNGNRLTVLAWVAFQPGFFLGRLFLF
                     RNPWCCDCRLEWLRDWMEGSGRVTDVPCASPGSVAGLDLSQVTFGRSSDGLCVDPEEL
                     NLTTSSPGPSPEPAATTVSRFSSLLSKLLAPRVPVEEAANTTGGLANASLSDSLSSRG
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BASE COUNT      379 a    749 c    750 g    419 t
ORIGIN
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Query Match 100.0%; Score 2297; DB 9; Length 2297;
Best Local Similarity 100.0%; Pred. No. 1.1e-258;
Matches 2297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 ggggtcccacggctgggtggtcctaagccactgggtggatgaaaggccgagggatgttgg 120
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Qy    241 gcgaccgcgcgggcctcctgcgggtgccggccgagctcccgtgcgaggcggtctccatcg 300
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Qy    301 acctggaccggaacggcctgcgcttcctgggcgagcgagccttcggcacgctgccgtcct 360
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Qy    661 acctggagcgcggccgcatcgaggcggtggcctccagctcgctgcagggcctgcgccgcc 720
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Qy    721 tgcgctcgctcagcctgcaggccaaccgcgtccgtgccgtgcacgctggcgccttcgggg 780
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RESULT 2
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DEFINITION Homo sapiens mRNA for leucine-rich repeat protein (CLRP gene).
ACCESSION AJ278865
VERSION AJ278865.1 GI:11877211
KEYWORDS CLRP gene; leucine-rich repeat protein.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2713)
AUTHORS Pusch,C.M., Zeitz,C., Brandau,O., Pesch,K., Achatz,H., Feil,S., Scharfe,C., Maurer,J., Jacobi,F.K., Pinckers,A., Andreasson,S., Hardcastle,A., Wissinger,B., Berger,W. and Meindl,A.
TITLE The complete form of X-linked congenital stationary night blindness is caused by mutations in a gene encoding a leucine-rich repeat protein
JOURNAL Nat. Genet. 26 (3), 324-327 (2000)
MEDLINE 20517341
REFERENCE 2 (bases 1 to 2713)
AUTHORS Pusch,C.M.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) Medical Genetics, Ludwigs Maximilians University, Goethestr. 29, Munich D-80336, GERMANY
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LRELAAFDNLFRRVPGALRGLANLTHAHLERGRIEAVASSSLQGLRRLRSLSLQANRV
RAVHAGAFGDCGVLEHLLLNDNLLAELPADAFRGLRRLRTLNLGGNALDRVARAWFAD
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BASE COUNT 470 a 841 c 864 g 538 t
ORIGIN

Query Match 97.6%; Score 2241; DB 9; Length 2713;
Best Local Similarity 100.0%; Pred. No. 3.3e-252;
Matches 2241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     57 ggtaggggtcccacggctgggtggtcctaagccactgggtggatgaaaggccgagggatg 116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    415 GGTAGGGGTCCCACGGCTGGGTGGTCCTAAGCCACTGGGTGGATGAAAGGCCGAGGGATG 474

Qy    117 ttggtcctgcttctgcatgcggtggtcctcggcctgcccagcgcctgggccgtgggggcc 176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    475 TTGGTCCTGCTTCTGCATGCGGTGGTCCTCGGCCTGCCCAGCGCCTGGGCCGTGGGGGCC 534

Qy    177 tgcgcccgcgcttgtcccgccgcctgcgcctgcagcaccgtggagcgcggctgctcggtg 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    535 TGCGCCCGCGCTTGTCCCGCCGCCTGCGCCTGCAGCACCGTGGAGCGCGGCTGCTCGGTG 594

Qy    237 cgctgcgaccgcgcgggcctcctgcgggtgccggccgagctcccgtgcgaggcggtctcc 296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    595 CGCTGCGACCGCGCGGGCCTCCTGCGGGTGCCGGCCGAGCTCCCGTGCGAGGCGGTCTCC 654

Qy    297 atcgacctggaccggaacggcctgcgcttcctgggcgagcgagccttcggcacgctgccg 356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    655 ATCGACCTGGACCGGAACGGCCTGCGCTTCCTGGGCGAGCGAGCCTTCGGCACGCTGCCG 714

Qy    357 tccttgcgccgcctgtcgctgcgccacaacaacctgtccttcatcacgcccggcgccttc 416
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    715 TCCTTGCGCCGCCTGTCGCTGCGCCACAACAACCTGTCCTTCATCACGCCCGGCGCCTTC 774

Qy    417 aagggcctgccgcgcctggctgagctgcgcctggcgcacaacggcgacctgcgctacctg 476
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    775 AAGGGCCTGCCGCGCCTGGCTGAGCTGCGCCTGGCGCACAACGGCGACCTGCGCTACCTG 834

Qy    477 cacgcgcgcaccttcgcggcgctcagccgcctgcgccgcctagacctagcagcctgccgc 536
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    835 CACGCGCGCACCTTCGCGGCGCTCAGCCGCCTGCGCCGCCTAGACCTAGCAGCCTGCCGC 894

Qy    537 ctcttcagcgtgcccgagcgcctcctggccgaactgccggccctgcgcgaactcgccgcc 596
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    895 CTCTTCAGCGTGCCCGAGCGCCTCCTGGCCGAACTGCCGGCCCTGCGCGAACTCGCCGCC 954

Qy    597 ttcgacaacctgttccgccgcgtgccgggcgcgctgcgcggcctggccaacctgacgcac 656
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    955 TTCGACAACCTGTTCCGCCGCGTGCCGGGCGCGCTGCGCGGCCTGGCCAACCTGACGCAC 1014

Qy    657 gcgcacctggagcgcggccgcatcgaggcggtggcctccagctcgctgcagggcctgcgc 716
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1015 GCGCACCTGGAGCGCGGCCGCATCGAGGCGGTGGCCTCCAGCTCGCTGCAGGGCCTGCGC 1074

Qy    717 cgcctgcgctcgctcagcctgcaggccaaccgcgtccgtgccgtgcacgctggcgccttc 776
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